

SEQUENCE LISTING

<110> Presnell, Scott R.
Taft, David W.

<120> A New Member of the Human
Syntaxin/Epimorphin Family

<130> 98-69

<160> 9

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1274

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (189)...(1049)

<400> 1

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gcggccgcgg cggcgcggag ctcgggcggc cgtggaggaa ctcagcctcg gccgcaggag      60
gcgccgggag cggagccgcc gggagtcgcg caacagggtt cttctccat cgtgcgccc      120
acaggggacg cgccctgc cgggagaggg gcttctcggg tcgcactctc gctcccagtc      180
caggcaaa atg aaa gac cgg cta gca gaa ctt ctg gac ttg tcc aag caa      230
      Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln
          1              5              10
```

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tat gac cag cag ttc cca gac ggg gac gat gag ttt gac tcg ccc cac      278
Tyr Asp Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His
    15              20              25              30
```

```
gag gac atc gtg ttc gag acg gac cac atc ctg gag tcc ctg tac cga      326
Glu Asp Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg
          35              40              45
```

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gac atc cgg gac att cag gat gaa aac cag ctg ctg gtg gcc gac gtg      374
Asp Ile Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val
          50              55              60
```

```
aag cgg ctg gga aag cag aac gcc cgc ttc ctc acg tcc atg cgg cgc      422
```

Lys Arg Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg	
65 70 75	
ctc agc agc atc aag cgc gac acc aac tcc atc gcc aag gcc atc aag	470
Leu Ser Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys	
80 85 90	
gcc cgg ggc gag gtc atc cac tgc aag ctg cgc gcc atg aag gag ctg	518
Ala Arg Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu	
95 100 105 110	
agc gag gcg gct gag gcc cag cac ggc ccg cac tcg gca gtg gcg cgc	566
Ser Glu Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg	
115 120 125	
att tcg cgg gcg cag tac aac gcg ctc acc ctc acc ttc cag cgc gcc	614
Ile Ser Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala	
130 135 140	
atg cac gac tac aac cag gcc gag atg aag cag cgc gac aac tgc aag	662
Met His Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys	
145 150 155	
atc cgc atc cag cgc cag ctg gag atc atg ggc aag gaa gtc tcg ggc	710
Ile Arg Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly	
160 165 170	
gac cag atc gag gac atg ttc gag cag ggt aag tgg gac gtg ttt tcc	758
Asp Gln Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser	
175 180 185 190	
gag aac ttg ctg gcc gac gtg aag ggc gcg cgg gcc gcc ctc aac gag	806
Glu Asn Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu	
195 200 205	
atc gag agc cgc cac cgc gaa ctg ctg cgc ctg gag agc cgc atc cgc	854
Ile Glu Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg	
210 215 220	
gac gta cac gag ctc ttc ttg cag atg gcg gtg ctg gtg gag aag cag	902
Asp Val His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln	
225 230 235	
gcc gac acc ctg aac gtc atc gag ctc aac gta caa aag acg gtc gac	950

Ala Asp Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp
 240 245 250

tac acc ggc cag gcc aag gcg cag gtg cgg aag gcc gtg cag tac gag 998
 Tyr Thr Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu
 255 260 265 270

gag aag aac ccc tgc cgg acc ctc tgc tgc ttc tgc tgt ccc tgc ctc 1046
 Glu Lys Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu
 275 280 285

aag tagcaggccg gcccgggccg ccaccgcccc tcccagacca tggagcgcgc 1099
 tgggaaggac gcaccaaagc cgggagctct gccctgcagg gagttgcccc aaccctttcc 1159
 ggaactcagt ctttagaaaa gaaacgccag gttcaagaat tgcaaaccag cctgtgcttg 1219
 gaaagatggg tagttgatac cgtccgatga ttcttcagta aagatagatt cccac 1274

<210> 2

<211> 287

<212> PRT

<213> Homo sapiens

<400> 2

Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
 1 5 10 15
 Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
 20 25 30
 Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
 35 40 45
 Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asp Val Lys Arg
 50 55 60
 Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
 65 70 75 80
 Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Arg
 85 90 95
 Gly Glu Val Ile His Cys Lys Leu Arg Ala Met Lys Glu Leu Ser Glu
 100 105 110
 Ala Ala Glu Ala Gln His Gly Pro His Ser Ala Val Ala Arg Ile Ser
 115 120 125
 Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
 130 135 140
 Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
 145 150 155 160
 Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
 165 170 175

Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
 180 185 190
 Leu Leu Ala Asp Val Lys Gly Ala Arg Ala Ala Leu Asn Glu Ile Glu
 195 200 205
 Ser Arg His Arg Glu Leu Leu Arg Leu Glu Ser Arg Ile Arg Asp Val
 210 215 220
 His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
 225 230 235 240
 Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
 245 250 255
 Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
 260 265 270
 Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu Lys
 275 280 285

<210> 3

<211> 861

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate sequence encodes the amino acid sequence of SEQ ID NO:2.

<221> variation

<222> (1)...(861)

<223> N is any nucleotide.

<400> 3

atgaargaym gnytnngnga rytnytnngay ytnwsnaarc artaygayca rcarttyccn	60
gayggngayg aygarttyga ywsnccncay gargayathg tnttygarac ngaycayath	120
ytngarwsny tntaymgnga yathmgngay athcargayg araaycaryt nytngtnngcn	180
gaygtnaarm gnytnngnaa rcaraaygcn mgnttyytna cnwsnatgmg nmgnytnwsn	240
wsnathaarm gngayacnaa ywsnathgcn aargcnatha argcnmgngg ngargtnath	300
caytgyaary tnmngngcnat gaargarytn wsngargcng cngargcnca rcayggncn	360
caywsngcng tngcnmgcnat hwsnmngcn cartayaayg cnytnacnyt nacnttycar	420
mgngcnatgc aygaytayaa ycargcngar atgaarcarm gngayaaytg yaarathmgn	480
athcarmgnc arytngarat hatgggnaar gargtnwsng gngaycarat hgargayatg	540
ttygarcarg gnaartggga ygtnttywsn garaayytny tngcngaygt naarggngcn	600
mgngcngcny tnaaygarat hgarwsnmgn caymgngary tnytnmgnyt ngarwsnmgn	660
athmgngayg tncaygaryt nttyytnear atggcngtny tngtngaraa rcargcngay	720
acnytnaayg tnathgaryt naaygtncar aaracngtny aytayacngg ncargcnaar	780
gcncargtnm gnaargcngt ncartaygar garaaraayc cntgymgnac nytntgytgy	840
ttytgytgyc cntgyytnaa r	861

<210> 4
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 4
 tggcgggtgct ggtggaga 18

<210> 5
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 5
 ccggcagggg ttcttctc 18

<210> 6
 <211> 287
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Lys Asp Arg Leu Ala Glu Leu Leu Asp Leu Ser Lys Gln Tyr Asp
 1 5 10 15
 Gln Gln Phe Pro Asp Gly Asp Asp Glu Phe Asp Ser Pro His Glu Asp
 20 25 30
 Ile Val Phe Glu Thr Asp His Ile Leu Glu Ser Leu Tyr Arg Asp Ile
 35 40 45
 Arg Asp Ile Gln Asp Glu Asn Gln Leu Leu Val Ala Asn Val Lys Arg
 50 55 60
 Leu Gly Lys Gln Asn Ala Arg Phe Leu Thr Ser Met Arg Arg Leu Ser
 65 70 75 80
 Ser Ile Lys Arg Asp Thr Asn Ser Ile Ala Lys Ala Ile Lys Ala Pro
 85 90 95
 Pro Glu Val Ile His Cys Asn Val Arg Ala Met Lys Glu Leu Ser Glu
 100 105 110
 Ala Ala Glu Ala Gln His Gly Pro Ala Leu Gly Ser Gly Gly Ile Ser
 115 120 125

Arg Ala Gln Tyr Asn Ala Leu Thr Leu Thr Phe Gln Arg Ala Met His
 130 135 140
 Asp Tyr Asn Gln Ala Glu Met Lys Gln Arg Asp Asn Cys Lys Ile Arg
 145 150 155 160
 Ile Gln Arg Gln Leu Glu Ile Met Gly Lys Glu Val Ser Gly Asp Gln
 165 170 175
 Ile Glu Asp Met Phe Glu Gln Gly Lys Trp Asp Val Phe Ser Glu Asn
 180 185 190
 Leu Leu Ala Asp Val Lys Gly Val Arg Ala Ala Leu Asn Glu Ile Glu
 195 200 205
 Ser Arg His Arg Glu Leu Val Arg Leu Glu Ser Ala Ile Arg Asp Val
 210 215 220
 His Glu Leu Phe Leu Gln Met Ala Val Leu Val Glu Lys Gln Ala Asp
 225 230 235 240
 Thr Leu Asn Val Ile Glu Leu Asn Val Gln Lys Thr Val Asp Tyr Thr
 245 250 255
 Gly Gln Ala Lys Ala Gln Val Arg Lys Ala Val Gln Tyr Glu Glu Lys
 260 265 270
 Asn Pro Cys Arg Thr Leu Cys Cys Phe Cys Cys Pro Cys Leu Lys
 275 280 285

<210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 7
 ggacgtgttt tccgagaact tg 22

<210> 8
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 8
 cgaccgtctt ttgtacgttg ag 22

<210> 9
 <211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker.

<400> 9

Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15